



ATG GAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTCACCCGAAGGGGAACACGCCA
TAC CTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGTGCGGT 70
M E T D A I D G Y I T C D N E L S P E G E H A
ATA TGGCCATTGACCTCACCTCAAGCACGCCCAATGGACAGCACGCCTCGCCAAGTCACATGACAAGCAC 140
TAT ACCGGTAACTGGAGTGGAGTTCGTGCGGGTTACCTGTCTGCGGAGCGGTTCAAGTGTACTGTTCTGTG
N M A I D L T S S T P N G Q H A S P S H M T S T
AAA TTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCTGAGCCGTGAGGATGAG 210
TTT AAGACATTTGACCTTTACGTCTCACTACTTCTCACACTGTCCGTGCGGGACTCGGCACTCCTACTC
N S V K L E M Q S D E E C D R Q P L S R E D E
ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCTAATTGAGAGCAGCGAGGTGGCCGACAACA 280
TAGTCCCCGGTGCTACTCCCTCGTGGGATCTTCTTGGGGATTAACTCTCGTCTCCACCGGCTGTTGT
I R G H D E G S S L E E P L I E S S E V A D N
GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350
CCTTTCAGGTCTTGAAGTTCGGCTCCCTCCTTAGGCCGAAGGCTTACCATTGACTTTACACTGCAGAC
R K V Q D L Q G E G G I R L P N G K L K C D V C
TGGCATGGTTTGCATTGGGCCCAATGTGCTTATGGTACATAAAAGGAGTCACACTGGTGAGCGGCCCTTC 420
ACCGTACCAAACGTAACCCGGGTACACGAATACCATGTATTTTCTCAGTGTGACCACTCGCCGGGAAG
G M V C I G P N V L M V H K R S H T G E R P F
CACTGTAACCAGTGCGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACAEATAAGTTACACTCTG 490
GTGACATTGGTCACGCCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGTATTTCAATGTGAGAC
H C N Q C G A S F T Q K G N L L R H I K L H S
GAGAGAAGCCCTTCAAATGTCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCT 560
CTCTCTTCGGGAAGTTTACAGGAAAGACATCGATACGAACATCTTCTTCCCTGCGAGAGTGTCTGTGGA
G E K P F K C P F C S Y A C R R R D A L T G H L
CAGGACCCATTCTGTGGGTAAACCTCACAAAGTGTAACTACTGTGGCCGAAGCTACAAGCAGCGCACGTCA 630
GTCCTGGGTAAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCTGTCGCGTGCAGT
R T H S V G K P H K C N Y C G R S Y K Q R T S

FIG. 3A

CTGGAGGAACACAAGGAACGCTGTCACAACCTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA 700
GACCTCCTTGTTGTTCTTGCGACAGTGTTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGT
L E E H K E R C H N Y L Q N V S M E A A G Q V
TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCT 770
ACTCAGTGGTACATGGCGGATACCTTCTAACATTCTTGTTCTCGGATAGTACCTGTTGTTATAAAGAGA
M S H H V P P M E D C K E Q E P I M D N N I S L
GGTGCCTTTTGAGAGACCTGCTGTCATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAGCTCCACT 840
CCACGGAAACTCTCTGGACGACAGTATCTCTCGAGTGCCGTTTATACCCTTTTCGCGTTTTTCGAGGTGA
V P F E R P A V I E K L T A N M G K R K S S T
CCTCAGAAGTTTGTTGGGGGAAAAGCTTATGCGATTGAGCTACCCAGATATTCATTTTGATATGAACTTAA 910
GGAGTCTTCAAACACCCCTTTTTCGAATACGCTAAGTCGATGGGTCTATAAGTAAACTATACTTGAATT
P Q K F V G E K L M R F S Y P D I H F D M N L
CATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTA 980
GTATACTCTTCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTTCGGTAGTTGTTACGTTAGTGGAT
T Y E K E A E L M Q S H M M D Q A I N N A I T Y
CCTTGGAGCTGAGGCCCTTCACCCTCTGATGCAGCATGCACCAAGCACAAATCGCTGAGGTGGCCCCAGTT 1050
GGAACCTCGACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTCTGTGTTAGCGACTCCACCGGGGTCAA
L G A E A L H P L M Q H A P S T I A E V A P V
ATAAGCTCAGCTTATTCTCAGGTCTATCATCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTG 1120
TATTCGAGTCGAATAAGAGTCCAGATAGTAGGTTTGTCTATCTTTCTGGGTAATCGTCCCTTTGTAGAC
I S S A Y S Q V Y H P N R I E R P I S R E T S
ATAGTCACGAAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAAGAGTCGACCCAGGAAAGAGA 1190
TATCAGTGCTTTTGTGTTGACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCCTTCTCT
D S H E N N M D G P I S L I R P K S R P Q E R E
GGCCTCGCCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCCTAC 1260
CCGGAGCGGGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTCAGGATG
A S P S N S C L D S T D S E S S H D D R Q S Y

FIG. 3B

CAAGGAAACCCTGCCTTAAATCCCAAGAGGAAACAAAGCCAGCTTACATGAAGGAGGATGTCAAGGCTT 1330
GTTCCTTTGGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTGCAATGTACTTCCTCCTACAGTTCCGAA
Q G N P A L N P K R K Q S P A Y M K E D V K A
TGGATGCTACCAAGGCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACAA 1400
ACCTACGATGGTTCCGGGGGTTCCCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCTCTTGT
L D A T K A P K G S L K D I Y K V F N G E G E Q
GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCATGTACACCATTACATG 1470
CTATTCCTCGGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTAC
I R A F K C E H C R V L F L D H V M Y T I H M
GGTTGCCATGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAAT 1540
CCAACGGTACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTA
G C H G Y R D P L E C N I C G Y R S Q D R Y E
TTTCATCACACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG 1598
AAAGTAGTGTGTAACAACCCCCGTCGTGTGTAAGGTGATCCGCAAACGTAAGGTTCC
F S S H I V G G Q H T F H A F A F Q G

FIG. 3C

ATGGAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTCACCCGAAGGGGAACACGCCA
TACCTTTGTCTGCGATAACTACCGATATATTGTACACTGTTACTCGAAAGTGGGCTTCCCCTTGTGCGGT 70
M E T D A I D G Y I T C D N E L S P E G E H A
ATATGGCCATTGACCTCACCTCAAGCACGCCCAATGGACAGCACGCCTCGCCAAGTCACATGACAAGCAC
TATACCGGTAACCTGGAGTGGAGTTCGTGCGGGTTACCTGTCGTGCGGAGCGGTTCAAGTGTACTGTTCTGTG 140
N M A I D L T S S T P N G Q H A S P S H M T S T
AAATTCTGTAAAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCTGAGCCGTGAGGATGAG
TTTAAGACATTTTCGACCTTTACGTCTCACTACTTCTCACACTGTCCGTGCGGGACTCGGCACTCCTACTC 210
N S V K L E M Q S D E E C D R Q P L S R E D E
ATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAACCCTAATTGAGAGCAGCGAGGTGGCCGACAACA
TAGTCCCCGGTGCTACTCCCCTCGTCGGATCTTCTTGGGGATTAAGTCTCGTCGCTCCACCGGCTGTTGT 280
I R G H D E G S S L E E P L I E S S E V A D N
GGAAAGTCCAGGACCTTCAAGGCGAGGGAGGAATCCGGCTTCCGAATGGTGAGCGGCCCTTCCACTGTAA
CCTTTCAGGTCTTGAAGTTCGGCTCCCTCCTTAGGCCGAAGGCTTACCACTCGCCGGAAGGTGACATT 350
R K V Q D L Q G E G G I R L P N G E R P F H C N
CCAGTGCGGAGCTTCTTTTACCCAGAAGGGCAACCTTCTGAGACACATAAAGTTACACTCTGGAGAGAAG
GGTCAGCCTCGAAGAAAATGGGTCTTCCCGTTGGAAGACTCTGTGATTTCAATGTGAGACCTCTCTTC 420
Q C G A S F T Q K G N L L R H I K L H S G E K
CCCTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCACAGGACACCTCAGGACCC
GGGAAGTTTACAGGAAAGACATCGATACGAACATCTTCTTCCCTGCGAGAGTGTCTGTGGAGTCTCTGGG 490
P F K C P F C S Y A C R R R D A L T G H L R T
ATTCTGTGGGTAAACCTCACAAGTGTAAGTGTGAGGCTACAAGCAGCGCACGTCACTGGAGGA
TAAGACACCCATTTGGAGTGTTCACATTGATGACACCGGCTTCGATGTTCTGTCGCGTGCAGTGACCTCCT 560
H S V G K P H K C N Y C G R S Y K Q R T S L E E
ACACAAGGAACGCTGTCACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCATGAGTCAC
TGTGTTCCCTGCGACAGTGTGATAGAGGTCTTACAGTCGTACCTCCGACGGCCCGTCCAGTACTCAGTG 630
H K E R C H N Y L Q N V S M E A A G Q V M S H

FIG. 4A

CATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATCATGGACAACAATATTTCTCTGGTGCCTT
GTACATGGCGGATACCTTCTAACATTCTTGTCTCGGATAGTACCTGTTGTTATAAAGAGACCACGGAA 700
H V P P M E D C K E Q E P I M D N N I S L V P
TTGAGAGACCTGCTGTCTATAGAGAAGCTCACGGCAAATATGGGAAAGCGCAAAGCTCCACTCCTCAGAA
AACTCTCTGGACGACAGTATCTCTTCGAGTGCCGTTTATACCCTTTCGCGTTTTTCGAGGTGAGGAGTCTT 770
F E R P A V I E K L T A N M G K R K S S T P Q K
GTTTGTGGGGGAAAAGCTTATGCGATTGAGCTACCCAGATATTCATTTTGATATGAACTTAACATATGAG
CAAACACCCCTTTTCGAATACGCTAAGTCGATGGGTCTATAAGTAAACTATACTTGAATTGTATACTC 840
F V G E K L M R F S Y P D I H F D M N L T Y E
AAGGAGGCTGAGCTGATGCAGTCTCATATGATGGACCAAGCCATCAACAATGCAATCACCTACCTTGGAG
TTCTCCGACTCGACTACGTCAGAGTATACTACCTGGTTCGGTAGTTGTTACGTTAGTGGATGGAACCTC 910
K E A E L M Q S H M M D Q A I N N A I T Y L G
CTGAGGCCCTTACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTTATAAGCTC
GACTCCGGGAAGTGGGAGACTACGTCGTACGTGGTTCTGTAGCGACTCCACCGGGGTCAATATTCGAG 980
A E A L H P L M Q H A P S T I A E V A P V I S S
AGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACCCATTAGCAGGGAAACATCTGATAGTCAC
TCGAATAAGAGTCCAGATAGTAGGTTTGTCTATCTTTCTGGGTAATCGTCCCTTTGTAGACTATCAGTG 1050
A Y S Q V Y H P N R I E R P I S R E T S D S H
GAAACAACATGGATGGCCCCATCTCTCTCATCAGACCAAAGAGTCGACCCAGGAAAGAGAGGCCTCGC
CTTTTGTGTACCTACCGGGGTAGAGAGAGTAGTCTGGTTTCTCAGCTGGGGTCCTTCTCTCCGGAGCG 1120
E N N M D G P I S L I R P K S R P Q E R E A S
CCAGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCGCCAGTCCTACCAAGGAAA
GGTCGTTATCGACGGAGCTAAGATGACTGAGTCTTTCATCGGTACTACTGGCGGTGAGGATGGTTCCTTT 1190
P S N S C L D S T D S E S S H D D R Q S Y Q G N
CCCTGCCTTAAATCCCAAGAGGAAACAAAGCCAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCT
GGGACGGAATTTAGGGTTCTCCTTTGTTTCGGGTGCAATGTACTTCTCTACAGTTCGAAACCTACGA 1260
P A L N P K R K Q S P A Y M K E D V K A L D A

FIG. 4B

ACCAAGGCCCCCAAGGGCTCTCTGAAGGACATCTATAAGGTTTTCAATGGAGAAGGAGAACAGATAAGGG
TGGTTCCGGGGGTTCCCGAGAGACTTCCTGTAGATATTCCAAAAGTTACCTCTTCCTCTTGTCTATTCCC 1330
T K A P K G S L K D I Y K V F N G E G E Q I R
CCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATGTCTGTACACCATTACATGGGTTGCCA
GGAAGTTCACACTCGTGACGGCTCAGGAAAAAGATCTGGTACAGTACATGTGGTAAGTGTACCCAACGGT 1400
A F K C E H C R V L F L D H V M Y T I H M G C H
TGGCTACCGGGACCCACTGGAATGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCA
ACCGATGGCCCTGGGTGACCTTACGTTGTAGACACCGATGTCTTCGGTCCTGGCGATGCTTAAAAGTAGT 1470
G Y R D P L E C N I C G Y R S Q D R Y E F S S
CACATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG
GTGTAACAACCCCCGTCGTGTGTAAGGTGATCCGCAAACGTAAGGTTCC 1520
H I V G G Q H T F H A F A F Q G

FIG. 4C

1/1	31/11
GCC CGG GCA GGT CGC ATT GCT ATA GCA CTG	ACT GAC CTC TCT CTC TCT CTT TTT TTT CCT
A R A G R I A I A L T D L S L S L F F P	
61/21	91/31
CTT TCC TGA AAC CCG ACA TTG TCA CCT CCT	CTT TGA GGG TTA GAA GAA GCT GAG ATC TCC
L S * N P T L S P P L * G L E E A E I S	
121/41	151/51
CGA CAG AGC TGG AAA TGG TGA TGA ATC TTT	TTT AAT CAA AGG ACA ATT TCT TTT CAT TGC
R Q S W K W * * I F F N Q R T I S F H C	
181/61	211/71
ACT TTG ACT ATG GAA ACA GAG GCT ATT GAT	GGC TAT ATA ACG TGT GAC AAT GAG CTT TCA
T L T M E T E A I D G Y I T C D N E L S	
241/81	271/91
CCC GAA AGG GAG CAC TCC AAT ATG GCA ATT	GAC CTC ACC TCA AGC ACA CCC AAT GGA CAG
P E R E H S N M A I D L T S S T P N G Q	
301/101	331/111
CAT GCC TCA CCA AGT CAC ATG ACA AGC ACA	GAT TCA GTA AAG CTA GAA ATG CAG AGT GAT
H A S P S H M T S T D S V K L E M Q S D	
361/121	391/131
GAA GAG TGT GAC AGG AAA CCC CTG AGC CGT	GAA GAT GAG ATC AGG GGC CAT GAT GAG GGT
E E C D R K P L S R E D E I R G H D E G	
421/141	451/151
AGC AGC CTA GAA GAA CCC CTA ATT GAG AGC	AGC GAG GTG GCT GAC AAC AGG GAA GTC CAG
S S L E E P L I E S S E V A D N R E V Q	
481/161	511/171
GAG CTT CAA GGC GAG GGA GGA ATC CGG CTT	CCG AAT GGT AAA CTG AAA TGT GAC GTC TGT
E L Q G E G G I R L P N G K L K C D V C	
541/181	571/191
GGC ATG GTT TGC ATT GGG CCC AAT GTG CTT	ATG GTA CAT AAA AGG AGT CAC ACT GGT GAA
G M V C I G P N V L M V H K R S H T G E	
601/201	631/211
CGC CCC TTC CAC TGT AAC CAG TGT GGA GCT	TCT TTT ACT CAG AAG GGC AAC CTT CTG AGA
R P F H C N Q C G A S F T Q K G N L L R	
661/221	691/231
CAC ATA AAG TTA CAC TCT GGA GAG AAG CCG	TTT AAA TGT CCT TTC TGT AGT CAC GCC TGT
H I K L H S G E K P F K C P F C S H A C	
721/241	751/251
AGA AGA AGG GAC GCC CTC ACA GGA TAC CTC	AGG ACC CAT TCT GTG GGT AAA CCT CAC AAG
R R R D A L T G Y L R T H S V G K P H K	
781/261	811/271
TGC AAC TAC TGT GGA CGA AGC TAC AAG CAG	CGC AGT TCA CTG GAG GAG CAC AAG GAA CGC
C N Y C G R S Y K Q R S S L E E H K E R	
841/281	871/291
TGC CAC AAC TAT CTC CAG AAT GTC AGC ATG	GAG GCT GCT GGG CAG GTC ATG AGT CAC CAT
C H N Y L Q N V S M E A A G Q V M S H H	
901/301	931/311
GTA CCT CCT ATG GAA GAT TGT AAG GAA CAA	GAG CCT ATT ATG GAC AAC AAT ATT TCT CTG
V P P M E D C K E Q E P I M D N N I S L	
961/321	991/331
GTG CCT TTT GAG AGA CCT GCT GTC ATA GAG	AAG CTC ACG GGG AAT ATG GGA AAA CGT AAA
V P F E R P A V I E K L T G N M G K R K	
1021/341	1051/351
AGC TCC ACT CCA CAA AAG TTT GTG GGG GAA	AAG CTC ATG CGA TTC AGC TAC CCA GAT ATT
S S T P Q K F V G E K L M R F S Y P D I	
1081/361	1111/371
CAC TTT GAT ATG AAC TTA ACA TAT GAG AAG	GAG GCT GAG CTG ATG CAG TCT CAT ATG ATG
H F D M N L T Y E K E A E L M Q S H M M	
1141/381	1171/391
GAC CAA GCC ATC AAC AAT GCA ATC ACC TAC	CTT GGA GCT GAG GCC CTT CAC CCT CTG ATG
D Q A I N N A I T Y L G A E A L H P L M	
1201/401	1231/411
CAG CAC CCG CCA AGC ACA ATC GCT GAA GTG	GCC CCA GTT ATA AGC TCA GCT TAT TCT CAG
Q H P P S T I A E V A P V I S S A Y S Q	

FIG. 5A

1261/421	1291/431
GTC TAT CAT CCA AAT AGG ATA GAA AGA CCC	ATT AGC AGG GAA ACT GCT GAT AGT CAT GAA
V Y H P N R I E R P	I S R E T A D S H E
1321/441	1351/451
AAC AAC ATG GAT GGC CCC ATC TCT CTC ATC	AGA CCA AAG AGT CGA CCC CAG GAA AGA GAG
N N M D G P I S L I	R P K S R P Q E R E
1381/461	1411/471
GCC TCT CCC AGC AAT AGC TGC CTG GAT TCC	ACT GAC TCA GAA AGC AGC CAT GAT GAC CAC
A S P S N S C L D S	T D S E S S H D D H
1441/481	1471/491
CAG TCC TAC CAA GGA CAC CCT GCC TTA AAT	CCC AAG AGG AAA CAA AGC CCA GCT TAC ATG
Q S Y Q G H P A L N	P K R K Q S P A Y M
1501/501	1531/511
AAG GAG GAT GTC AAA GCT TTG GAT ACT ACC	AAG GCT CCT AAG GGC TCT CTG AAG GAC ATC
K E D V K A L D T T	K A P K G S L K D I
1561/521	1591/531
TAC AAG GTC TTC AAT GGG GAA GGA GAA CAG	ATT AGG GCC TTC AAG TGT GAG CAC TGC CGA
Y K V F N G E G E Q	I R A F K C E H C R
1621/541	1651/551
GTC CTT TTC CTA GAC CAT GTC ATG TAC ACC	ATT CAC ATG GGT TGC CAT GGC TAC CGG GAC
V L F L D H V M Y T	I H M G C H G Y R D
1681/561	1711/571
CCA CTG GAA TGT AAC ATC TGT GGC TAC AGA	AGC CAG GAC CGT TAT GAG TTT TCA TCA CAC
P L E C N I C G Y R	S Q D R Y E F S S H
1741/581	1771/591
ATT GTT CGA GGG GAG CAC ACA TTC CAC TAG	GCC TTT TCA TTC CAA AGG GGA CCC TAT GAA
I V R G E H T F H *	A F S F Q R G P Y E
1801/601	1831/611
GTA AAG ACT GCA CAT GAA GAA ATA CTG CAC	TTA CAA TCC CAC CTT TCC TCA AAT GTT GTA
V K T A H E E I L H	L Q S H L S S N V V
1861/621	1891/631
CCT TTT ATT TTT TTA ATA TAA TAC TGG TGA	TAA TCT TAT TTT GTG GAG CAG TGT CAT TTG
P F I F L I * Y W * *	S Y F V E Q C H L
1921/641	
CTC TGC T	
L C	

FIG. 5B

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1  ATGGAAACAGACGCTATTGATGGCTATATAACATGTGACAATGAGCTTTC 50
   |||
190 ATGGAAACAGAGGCTATTGATGGCTATATAACGTGTGACAATGAGCTTTC 239
   |||
51  ACCCGAAGGGGAACACGCCAATATGGCCATTGACCTCACCTCAAGCACGC 100
   |||
240 ACCCGAAGGGGAGCACTCCAATATGGCAATTGACCTCACCTCAAGCACAC 289
   |||
101 CCAATGGACAGCAcGCCTCGCCAAGTCACATGACAAGCACAAATTCTGTA 150
   |||
290 CCAATGGACAGCATGCCTCACCAAGTCACATGACAAGCACAGATTTCAGTA 339
   |||
151 AAGCTGGAAATGCAGAGTGATGAAGAGTGTGACAGGCAGCCCCTGAGCCG 200
   |||
340 AAGCTAGAAATGCAGAGTGATGAAGAGTGTGACAGGAAACCCCTGAGCCG 389
   |||
201 TGAGGATGAGATCAGGGGCCACGATGAGGGGAGCAGCCTAGAAGAcCCC 250
   |||
390 TGAAGATGAGATCAGGGGCCATGATGAGGGTAGCAGCCTAGAAGAACCCC 439
   |||
251 TAATTGAGAGCAGCGAGGTGGCCGACAACAGGAAAGTCCAGGACCTTCAA 300
   |||
440 TAATTGAGAGCAGCGAGGTGGCTGACAACAGGGAAGTCCAGGAGCTTCAA 489
   |||
301 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 350
   |||
490 GGCGAGGGAGGAATCCGGCTTCCGAATGGTAAACTGAAATGTGACGTCTG 539
   |||
351 TGGCATGGTTTGCATTGGGCCCCAATGTGCTTATGGTACATAAAAGGAGTC 400
   |||
540 TGGCATGGTTTGCATTGGGCCCCAATGTGCTTATGGTACATAAAAGGAGTC 589
   |||
401 AACTGGTGAGCGGCCCTTCCACTGTAACCAGTGCGGAGCTTCTTTTACC 450
   |||
590 AACTGGTGAAACGCCCTTCCACTGTAACCAGTGCGGAGCTTCTTTTACT 639
   |||
451 CAGAAGGGCAACCTTCTGAGACACATAAAGTTAACTCTGGAGAGAAGCC 500
   |||
640 CAGAAGGGCAACCTTCTGAGACACATAAAGTTAACTCTGGAGAGAAGCC 689
   |||
501 CTTCAAATGTCCTTTCTGTAGCTATGCTTGTAGAAGAAGGGACGCTCTCA 550
   |||
690 GTTCAAATGTCCTTTCTGTAGTCACGCCTGTAGAAGAAGGGACGCCCTCA 739
   |||
551 CAGGACACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGTAAGTAC 600
   |||
740 CAGGATACCTCAGGACCCATTCTGTGGGTAAACCTCACAAGTGCAAGTAC 789
   |||
601 TGTGGCCGAAGCTACAAGCAGCGCACGTCACTGGAGGAACACAAGGAACG 650
   |||
790 TGTGGACGAAGCTACAAGCAGCGCAGTTCACTGGAGGAGCACAAGGAACG 839
   |||
651 CTGTCACAACTATCTCCAGAATGTCAGCATGGAGGCTGCCGGGCAGGTCA 700
   |||
840 CTGCCACAACCTATCTCCAGAATGTCAGCATGGAGGCTGCTGGGCAGGTCA 889
   |||
701 TGAGTCACCATGTACCGCCTATGGAAGATTGTAAGGAACAAGAGCCTATC 750
   |||
890 TGAGTCACCATGTACCTCCTATGGAAGATTGTAAGGAACAAGAGCCTATT 939
   |||
751 ATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGA 800
   |||

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FIG. 6A

940 ATGGACAACAATATTTCTCTGGTGCCTTTTGAGAGACCTGCTGTCATAGA 989
 801 GAAGCTCACGGCAAATATGGGAAAGCGCAAAGCTCCACTCCTCAGAAGT 850
 |||||
 990 GAAGCTCACGGGGAATATGGGAAAACGTAAAAGCTCCACTCCACAAAAGT 1039
 851 TTGTGGGGGAAAAGCTTATGCGATTGAGCTACCCAGATATTCATTTTGAT 900
 |||||
 1040 TTGTGGGGGAAAAGCTCATGCGATTGAGCTACCCAGATATTCATTTTGAT 1089
 901 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 950
 |||||
 1090 ATGAACTTAACATATGAGAAGGAGGCTGAGCTGATGCAGTCTCATATGAT 1139
 951 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1000
 |||||
 1140 GGACCAAGCCATCAACAATGCAATCACCTACCTTGGAGCTGAGGCCCTTC 1189
 1001 ACCCTCTGATGCAGCATGCACCAAGCACAATCGCTGAGGTGGCCCCAGTT 1050
 |||||
 1190 ACCCTCTGATGCAGCACCCGCAAGCACAATCGCTGAAGTGGCCCCAGTT 1239
 1051 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAACAGGATAGAAAGACC 1100
 |||||
 1240 ATAAGCTCAGCTTATTCTCAGGTCTATCATCCAAATAGGATAGAAAGACC 1289
 1101 CATTAGCAGGGAAACATCTGATAGTCACGAAAACAACATGGATGGCCCCA 1150
 |||||
 1290 CATTAGCAGGGAAACTGCTGATAGTCATGAAAACAACATGGATGGCCCCA 1339
 1151 TCTCTCTCATCAGACCAAAGAGTCGACCCCAAGGAAAGAGAGGCCTCGCCC 1200
 |||||
 1340 TCTCTCTCATCAGACCAAAGAGTCGACCCCAAGGAAAGAGAGGCCTCTCCC 1389
 1201 AGCAATAGCTGCCTCGATTCTACTGACTCAGAAAGTAGCCATGATGACCG 1250
 |||||
 1390 AGCAATAGCTGCCTGGATTCCACTGACTCAGAAAGCAGCCATGATGACCA 1439
 1251 CCAGTCCTACCAAGGAAACCCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1300
 |||||
 1440 CCAGTCCTACCAAGGACACCCCTGCCTTAAATCCCAAGAGGAAACAAAGCC 1489
 1301 CAGCTTACATGAAGGAGGATGTCAAGGCTTTGGATGCTACCAAGGCCCCC 1350
 |||||
 1490 CAGCTTACATGAAGGAGGATGTCAAAGCTTTGGATACTACCAAGGCTCCT 1539
 1351 AAGGGCTCTCTGAAGGACATCTATAAGGTTTCAATGGAGAAGGAGAACA 1400
 |||||
 1540 AAGGGCTCTCTGAAGGACATCTACAAGGTCTTCAATGGGGAAGGAGAACA 1589
 1401 GATAAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTTCTAGACCATG 1450
 |||||
 1590 GATTAGGGCCTTCAAGTGTGAGCACTGCCGAGTCCTTTTCTAGACCATG 1639
 1451 TCATGTACACCATTACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1500
 |||||
 1640 TCATGTACACCATTACATGGGTTGCCATGGCTACCGGGACCCACTGGAA 1689
 1501 TGCAACATCTGTGGCTACAGAAGCCAGGACCGCTACGAATTTTCATCACA 1550
 |||||
 1690 TGTAACATCTGTGGCTACAGAAGCCAGGACCGTTATGAGTTTTTCATCACA 1739
 1551 CATTGTTGGGGGGCAGCACACATTCCACTAGGCGTTTGCATTCCAAGG 1598
 |||||
 1740 CATTGTTGAGGGGAGCACACATTCCACTAGGCCTTTTCATTCCAAGG 1787

FIG. 6B

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1  METEAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASP SHMTSTDSV 50
  |||
1  METEAIDGYITCDNELSPEREHSNMAIDLTSSTPNGQHASP SHMTSTDSV 50
  |||
51  KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
  |||
51  KLEMQSDEECDRKPLSREDEIRGHDEGSSLEEPLIESSEVADNREVQELQ 100
  |||
101 GEGGIRLPNGKCLKDVCGMVCIGPNVLMVHKRSHTGERPFHCNQCASFT 150
  |||
101 GEGGIRLPNGKCLKDVCGMVCIGPNVLMVHKRSHTGERPFHCNQCASFT 150
  |||
151 QKGNLLRHIKLSHGEKPFKCPFCSHACRRRDALTGYLRTHSVGKPHKCNV 200
  |||
151 QKGNLLRHIKLSHGEKPFKCPFCSHACRRRDALTGYLRTHSVGKPHKCNV 200
  |||
201 CGRSYKQRSSLEE HKERCHNYLQNVSM EAAGQVMSHHVPPMEDCKEQEPI 250
  |||
201 CGRSYKQRSSLEE HKERCHNYLQNVSM EAAGQVMSHHVPPMEDCKEQEPI 250
  |||
251 MDNNISLVPFERPAVIEKLTGNMGKRKSSTPQKFVGEKLMRFSYPDIHFD 300
  |||
251 MDNNISLVPFERPAVIEKLTGNMGKRKSSTPQKFVGEKLMRFSYPDIHFD 300
  |||
301 MNLTYEKEAELMQSHMMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
  |||
301 MNLTYEKEAELMQSHMMDQAINNAITYLGAEALHPLMQHPPSTIAEVAPV 350
  |||
351 ISSAYSQVYHPNRIERPISRETADSHENNM DGPISLIRPKSRPQEREASP 400
  |||
351 ISSAYSQVYHPNRIERPISRETADSHENNM DGPISLIRPKSRPQEREASP 400
  |||
401 SNSCLDSTDSESSHDDHQS YQGHPALNPKRKQSPAYMKEDVKALDTTKAP 450
  |||
401 SNSCLDSTDSESSHDDHQS YQGHPALNPKRKQSPAYMKEDVKALDTTKAP 450
  |||
451 KGSLKDIYKVFNGEGEQIRAFKCEHCRVLF LDHVMYTIHMGCHGYRDPLE 500
  |||
451 KGSLKDIYKVFNGEGEQIRAFKCEHCRVLF LDHVMYTIHMGCHGYRDPLE 500
  |||
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526
  |||
501 CNICGYRSQDRYEFSSHIVRGEHTFH 526
  |||

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FIG. 7